autodicity 7

SEQUENCE LISTING

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 Imboden, Martin
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 Miescher, Sylvia
 Vogel, Monique
 Amstutz, Hanspeter



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TECH CENTER 1600/2900

<120> POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS, THE DNA ENCODING THEM AND THE PROCESS FOR THEIR PREPARATION AND USE

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TECH CENTER 1600/2900

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- <141> 1999-01-21
- <150> PCT/EP97/03253
- <151> 1997-06-20
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- <151> 1996-06-24
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Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser 50 60

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu 65 70 75 80

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ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 60

aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr

65 70 75 80 ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 <210> 26 <211> 125 <212> PRT <213> Homo sapiens <400> 26 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser <210> 27 <211> 312 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(312) <400> 27 gtg atg acc cag tot cca too too ctg tot gca tot gta gga gac aga Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

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aca Thr	tcc Ser 50	agt Ser	ttg Leu	caa Gln	agt Ser	ggg Gly 55	gtc Val	cca Pro	tca Ser	agg Arg	ttc Phe 60	agt Ser	ggc Gly	agt Ser	gga Gly	192
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Trp	Tyr	Gln 35	Gln	Lys	Pro	Gly	Lys 40	Ala	Pro	Lys	Leu	Leu 45	Ile	Tyr	Ala	
Thr	Ser 50	Ser	Leu	Gln	Ser	Gly 55	Val	Pro	Ser	Arg	Phe 60	Ser	Gly	Ser	Gly	
Ser 65	Gly	Thr	Asp	Phe	Thr 70	Leu	Thr	Ile	Asn	Ser 75	Leu	Gln	Pro	Glu	Asp 80	
Phe	_		_		a	Gln	Gln	Ser	Tyr	Thr	Thr	Pro	Ser	Phe	Gly	
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Gly	Met	His 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val	
Ala	Phe 50	Ile	Trp	Phe	Asp	Gly 55	Ser	Asn	Lys	Gly	Tyr 60	Val	Asp	Ser	Val	
Lys 65	Gly	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ser 75	Lys	Asn	Met	Leu	Tyr 80	
Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys	
Ala	Arg	Glu	Lys	Ala	Leu	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Leu	

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<213> Homo sapiens

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ctc Leu	gta Val	ttc Phe	ggc Gly 100	gga Gly	ggg Gly	acc Thr	aag Lys	ctg Leu 105	acc Thr	gtc Val	cta Leu	cgt Arg	cag Gln 110	ccc Pro		3
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Glu	Asp	Glu	Ala	Glu 85	Tyr	Tyr	Сув	Leu	Leu 90	Tyr	Tyr	Gly	Gly	Ala 95	Gln	
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gcg Ala	aga Arg	gac Asp	aag Lys 100	gcg Ala	gtt Val	cgg Arg	gga Gly	att Ile 105	agc Ser	agg Arg	tac Tyr	aac Asn	tat Tyr 110	tac Tyr	atg Met	336
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Ala	Arg	Asp	Lys 100	Ala	Val	Arg	Gly	Ile 105	Ser	Arg	Tyr	Asn	Tyr 110	Tyr	Met	
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gtg ttg acc cag tct cca tcc tcc ctg tct gca tct ata cga gac aga Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg

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Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg

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ctg Leu	caa Gln	atg Met	aac Asn	ggc Gly 85	ctg Leu	aga Arg	gcc Ala	gaa Glu	gac Asp 90	acg Thr	gct Ala	gta Val	tat Tyr	tat Tyr 95	tgt Cys	288
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Lys 65	Gly	Arg	Phe	Thr	Val 70		Arg	Asp	Asn	Ser 75		Asn	Thr	Leu	Tyr 80	
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35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly 55 50 Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys <210> 45 <211> 375 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(375) cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48 Gln Val Lys Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly tee etq aga etc tee tgt gta geg tet gga tte ace tte agg agt tat 96 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 144 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 192 gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 240 aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac acg ctc tat Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 288 ctg caa atg aag agc ctg aga gcc gag gac acg gct gta tat tat tgt Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 336 gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 105 gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120

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288

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50 55 60

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Leu	Gln	Met	Lys	Ser 85	Leu	Arg	Ala	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys	
Ala	Arg	Glu	Lys 100	Ala	Leu	Arg	Gly	Ile 105	Ser	Arg	Tyr	Asn	Tyr 110	Tyr	Leu	
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tgg Trp	tat Tyr	cag Gln 35	cag Gln	aaa Lys	cca Pro	Gly 999	aaa Lys 40	gcc Ala	cct Pro	aag Lys	ctc Leu	ctg Leu 45	atc Ile	tat Tyr	gct Ala	144
gca Ala	tcc Ser 50	agt Ser	ttg Leu	caa Gln	agt Ser	999 Gly 55	gtc Val	cca Pro	tca Ser	agg Arg	ttc Phe 60	agt Ser	ggc Gly	agt Ser	gga Gly	192
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	atg Met			_	_	_	_			_		_				144

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